Phylogeny and the Tree of Life

Overview: Investigating the Tree of Life

- Classification is the grouping of organisms based on similar features. Systematics is the discipline of the classification of organisms and determines their evolutionary relationships. Systematists use fossil, molecular, and genetic data to infer evolutionary relationships.
- **Taxonomy** is the ordered division and naming of organisms. In other words, taxonomy is the science of studying classification. It looks at features and tries to arrange them in a logical order.

- **Species**
- «a group of living organisms which have been inhabiting a particular habitat for a certain period, consisting of similar individuals capable of exchanging genes or interbreeding. Their biochemical, behavioral and physiological responses are similar when exposed to similar environmental conditions»

Using *common names can be very confusing* because there are usually multiple *different names* given to the same organism using *different languages* that are not known to everyone.

Tench (English)
Suder (Flemish)
Schlei (German)
Kadife (Turkish)

- Scientific names are unique to only one type of organism and use Latin so that no matter what country a scientist is from or what language they speak, they will understand each other.

Canis lupus L., 1758

- The first letter of the genus is capitalized, and the entire species name is written in italics.
- Both parts together name the species. This is the species specific epithet.

Hierarchical Classification

- Linnaeus introduced a system for grouping species in increasingly broad categories.
- A ‘species’ is the fundamental taxon. Groups of similar species form the next largest taxon called a ‘genus’. Groups of similar genera form the next largest taxon called a ‘family’ …and so on, up to the largest taxon = **Domain**.
- The taxonomic groups from broad to narrow are, **domain**, **kingdom**, **phylum**, **class**, **order**, **family**, **genus**, and **species.**
- A taxonomic unit at any level of this hierarchy is called a **taxon.**

Classification and Phylogeny

- **Phylogeny** is the evolutionary history of a species or group of related species.
- Systematists investigate the evolutionary relationships using branched **phylogenetic trees.**
- A phylogenetic tree represents a hypothesis about evolutionary relationships, including a common ancestor and all its descendents.
- A phylogenetic tree is a family tree that shows a hypothesis about the evolutionary relationships thought to exist among groups of organisms. It does not show the actual evolutionary history of organisms.

Phylogenetic trees are usually based on a combination of these lines of evidence:

- **Fossil records**
- **Morphology**
- **Embryological patterns of development**
- **Chromosomes and DNA**

Fossil records

- The fossil records often provide clues to evolutionary relationships
- It cannot be read like a story book because some fossil records are incomplete
- Systematic taxonomists consider other evidences to confirm the information contained within the fossil record with other lines of evidence.

Morphology

Taxonomists study an organism's morphology and compare it to other living organisms.

Homologous features are important. But it is important to separate features that are **truly** homologous with those that seem homologous but are actually analogous.

The more homologous features two organisms share, the more closely related they are thought to be.

Embryological Patterns of Development

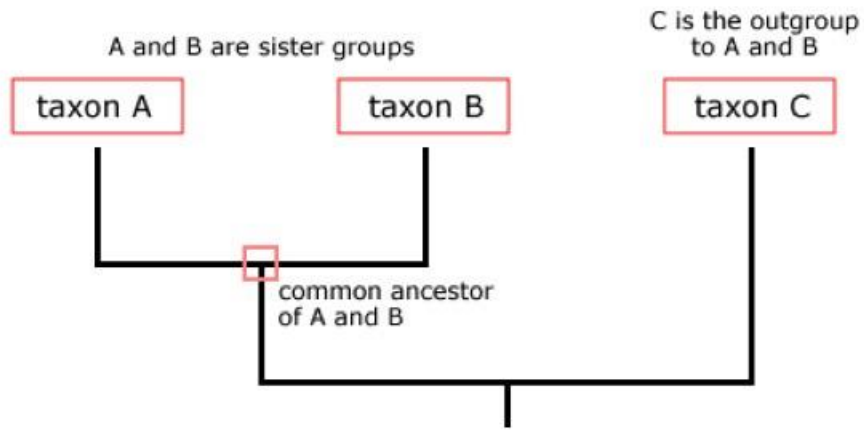
Early pattern in embryological development provide evidences for phylogenetic relationships.
They are also useful for testing hypotheses about relationships that have developed from other lines of evidence.

Chromosomes and Macromolecules

Organisms with similar morphologies or DNA sequences are likely to be more closely related than organisms with different structures or sequences.

Scientists compare amino acid sequences for homologous protein molecules of different species. The number of amino acid differences are clue to how long ago two species diverged from a shared evolutionary ancestor.

- Phylogeny
- Each **branch point** represents the divergence of two species (or taxons).
- **Sister taxa** are groups that share a common ancestor.



- Phylogenetic trees do show patterns of descent.
- Phylogenetic trees do not indicate when species evolved or how much genetic change occurred in a lineage.
- It shouldn't be assumed that a taxon evolved from the taxon next to it.
- *Phylogeny provides important information about **similar characteristics** in closely related species.*

When constructing a phylogeny, systematists need to distinguish whether a similarity is the result of homology or analogy.

- ***Homology*** is *similarity due to* ***shared ancestry***.

A character state that is shared between two taxa maybe so because they inherited it from a common ancestor, or it is **HOMOLOGOUS** (a homology/ synapomorphy).

«a fundamental similarity based on common descent».

- ***Analogy*** is *similarity due to* ***convergent evolution***.

The shared character might occur because they were evolved independently, in which case they are called a **Analogous.**

WHAT IS HOMOPLASY? (=ANALOGY)

Homoplasy, describes a feature that two or more different species have in common that was not inherited from their recent ancestor.

The fins of a whale and the fins of a shark are examples of homoplasy due to convergence, the independent acquisition of a character in different lineages.

- Homology can be distinguished from analogy by comparing fossil evidence and the degree of complexity. The more complex two similar structures are, the more likely it is that they are homologous.
- Once homologous characters have been identified, they can be used to build a phylogenetic tree.

Cladistics groups organisms by common descent

Cladistics is a system of taxonomy that reconstructs phylogenies by inferring relationships based on similarities. Or in other words; cladistics is a method to generate phylogenetic trees.

It focuses on a set of unique traits found in a particular group of organisms. These unique features are called derived traits or derived characters.

Using patterns of shared derived traits, biologists used cladistics to construct a branching diagram called a cladogram.
A cladogram shows show a sequence in which different groups of organisms evolved.

- A **clade** is a group of species that includes an ancestral species and all its descendants.

- A **monophyletic** group consists of the ancestor species and all its descendants.
- A **paraphyletic** group consists of an ancestral species and some of the descendants.
- A **polyphyletic** group consists of various species that lack a common ancestor.

Shared Ancestral and Shared Derived Characters

- In comparison with its ancestor, an organism has both shared and different characteristics.
- A **shared ancestral character** is a character that originated in an ancestor of the taxon.
- A **shared derived character** is an evolutionary novelty, unique feature for a particular clade.

Animal Diversity

Animals - Overview

In this chapter we will explain the characteristics that all animals share, as well as the evolutionary history of this kingdom.

Animals are multicellular, heterotrophic eukaryotes with tissues that develop from embryonic layers. But it should be kept in mind that it is difficult to get a list of the traits that all animals share. There are exceptions to nearly every criterion for distinguishing animals from other life-forms.

Animals - Structure

- *Nutritional Mode*: Animals are *heterotrophs* that *ingest* their food. (Plants? Fungi?)
- Animals are *multicellular* eukaryotes.
- Animal cells don't have *cell walls*. Instead their bodies are held together by *structural proteins,* located in the cell membrane, such as *collagen*.
- The cells of most animals are organized into **tissues**, groups of similar cells that act as a functional unit. For example, muscle tissue and nervous tissue are unique to animals. The ability to move and conduct nerve impulses underlies many of the adaptations that differentiate animals from plants and fungi.

Reproduction and Development

- Most animals *reproduce sexually*, with the *diploid stage* usually *dominating* the life cycle. In the haploid stage egg and sperm are produced by gonads.

- *After fertilization*, the *zygote* undergoes rapid cell division called ***cleavage*****.** During cleavage, a series of mitotic cell divisions occur without cell growth between the divisions.

- Cleavage leads to formation of a ***blastula*****.** The blastula (meaning "sprout") is a hollow sphere of cells, referred to as blastomeres, surrounding an inner fluid-filled cavity called the blastocoele formed during an early stage of embryonic development in animals.

The blastula undergoes ***gastrulation***. Gastrulation is an early phase in the embryonic development of most animals, forming a 3-layered structure known as the **gastrula**. Gastrula soon will form different *layers* of *embryonic tissues*.

The primary gut that forms during gastrulation in the developing zygote is known as the archenteron.

Although adult animals have a wide variation in morphology, the genes that control animal development are similar across a broad range of taxa. *All animals*, and only animals, have ***Hox* genes** that *regulate* the development of *body form*. Hox genes are responsible for the wide diversity of *animal morphology.*